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UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF WYOMING

UNITED STATES OF AMERICA,)	
)	
Plaintiff,)	
)	
v.)	No. 18-CR-020-SWS
)	
ARAPAHO JAMES OLDMAN,)	
)	
Defendant.)	

**DECLARATION OF DAN KRANE IN SUPPORT OF DEFENDANT OLDMAN'S
MOTION TO EXCLUDE EXPERT TESTIMONY ON STRMIX-
GENERATED DNA INCLUSION OR MATCH STATISTIC UNDER *DAUBERT* AND
FEDERAL RULES OF EVIDENCE 702**

I, DAN KRANE, declare the following:

BACKGROUND

1. I am a Professor of Biological Sciences (with a courtesy appointment in the Department of Computer Science) at Wright State University in Dayton Ohio. I have recently completed a one-year term as a fellow of the American Council on Education at the University of Notre Dame in Notre Dame, Indiana.

2. I have a B.S. degree with a double major in Biology and Chemistry from John Carroll University (Cleveland, Ohio), and a Ph.D. from the Biochemistry program of the Cell and Molecular Biology Department of the Pennsylvania State University (State College, Pennsylvania). I have conducted postdoctoral research using the tools of molecular biology to answer questions in the fields of population genetics and molecular evolution in the Genetics Department of the Washington University Medical School (St. Louis, Missouri) and in the Department of Organismic and Evolutionary Biology of Harvard University (Cambridge, Massachusetts).
3. I have published more than 50 scholarly papers on a variety of topics including population genetic studies of the genetic diversity of human populations at DNA typing loci, of organisms exposed to environmental stressors, and the use of DNA typing in forensic science. I am also the lead author of a widely used undergraduate textbook, *Fundamental Concepts of Bioinformatics*.
4. I was a founding member of and two-time gubernatorial appointee to the Commonwealth of Virginia's Scientific Advisory Committee, a 12-member panel established by statute to provide oversight and guidance to the Virginia Department of Forensic Science (the full-service crime laboratory for the Commonwealth of Virginia).
5. I have testified in more than 110 criminal proceedings that have involved forensic DNA typing (in 23 different state and district courts, several courts martial, and in three different Federal courts within the United States, a Coronial Inquest in the State of Victoria in Australia, in Belfast Crown Court in Northern Ireland, the Black Friar's Court and the Central Criminal Court of London and in Oxford Crown Court in England).
6. My curriculum vitae is attached as Exhibit A to this Declaration. Unless otherwise noted, I make this declaration based on my own personal knowledge. With respect to those matters not personally known to me, I make this declaration upon information and belief.

7. I was retained by the Office of the Federal Public Defender to review the FBI's STR DNA testing in the above-captioned case and to provide my opinions regarding items #12 and #53.
8. Materials I have received for my review include laboratory reports signed by Jaclyn Garfinkle of the FBI DNA Casework Unit and dated May 1, 2018; July 11, 2018; and September 12, 2018. I have received associated bench notes, electronic data files, and laboratory standard operating procedures. I have also received a 10-page FBI internal validation summary document entitled, "Validation of STRmix™ v2.4 for use with Globalfiler™ DNA Typing Results Generated on the 3500xL."
9. Motivation for conducting internal validation studies is described by the Scientific Working Group on DNA Analysis Methods (SWGDAM; Scientific Working Group on DNA Analysis Methods, "Guidelines for the Validation of Probabilistic Genotyping Systems," 2015. Available at -
https://docs.wixstatic.com/ugd/4344b0_22776006b67c4a32a5ffc04fe3b56515.pdf):

To identify data features (e.g., minimum quality requirements, number of contributors) that render a profile appropriate or inappropriate for probabilistic genotyping, the laboratory should test data across a range of characteristics that are representative of those typically encountered by the testing laboratory. Data should be selected to test the system's capabilities and to identify its limitations.

NUMBER OF CONTRIBUTORS

10. STRmix™ requires multiple inputs from its operator prior to mixture deconvolution. One input is a specification of the number of contributors of DNA to the sample being evaluated. It is widely accepted that the true number of contributors to a casework (questioned) sample cannot be known but that a lower bound can be reasonably estimated. Methods used to estimate numbers of contributors to mixtures vary in accuracy and reproducibility.
11. The FBI laboratory's stated method for estimating the number of contributors (DNA Procedures Manual 233-2) incorporates pairwise peak height ratio comparisons of peaks

within a locus but does not provide analysts with specific guidance regarding how the estimate should be made. And, the utility of information pertaining to peak height similarity/difference within a locus in determining the number of contributors to a sample quickly diminishes as the number of contributors to a sample increases. As such, it is not clear if and how peak height ratio information may have been used in an attempt to objectively determine the number of contributors to samples such as items 12 and 53 in this case.

12. By an almost universally relied upon allele counting approach, the presence of five or six labeled peaks at multiple loci suggests that the genotyping results of item 12 and item 53 are consistent with the presence of at least three contributors to these samples (not “three” or even “most likely three”). Based on peak height imbalances and low-level peaks, I agree that the genotyping results of item 12 and item 53 could be consistent with the presence of at least four contributors to each sample, however Jaclyn Garfinkle specifically instructed STRmix™ to perform deconvolutions of both items under the assumption that they both contained DNA from four (and only four) contributors.
13. Estimates regarding the number of contributors to a mixture are most reliable for the Globalfiler test kit for mixtures of up to only three contributors. When all alleles added to a sample from all contributors are observed in the testing results (and, in the absence of any other complicating factors and disregarding peak height imbalance information), known three-person mixtures have been shown to be underestimated as originating from two individuals in only 0.2% or fewer samples (M. D. Coble, J.-A. Bright, J. S. Buckleton, and J. M. Curran, “Uncertainty in the number of contributors in the proposed new CODIS set,” *Forensic Sci. Int. Genet.*, vol. 19, pp. 207–211, 2015). A recent study of samples of known origin (lab-made) by Bright, et al. demonstrated that no lab underestimated the number of contributors to known three-person mixtures [though 2% of three-person mixtures were incorrectly assumed to have originated from four contributors (see Figure 1; J. Bright, R. Richards, M. Kruijver, H. Kelly, C. McGovern, A.

Magee, A. Mcwhorter, A. Ciecko, B. Peck, C. Baumgartner, C. Buettner, S. McWilliams, C. McKenna, C. Gallacher, B. Mallinder, D. Wright, D. Johnson, D. Catella, E. Lien, C. O'Connor, G. Duncan, J. Bundy, J. Echard, J. Lowe, J. Stewart, K. Corrado, S. Gentile, M. Kaplan, M. Hassler, N. McDonald, P. Hulme, R. H. Oefelein, S. Montpetit, M. Strong, S. Noël, S. Malson, S. Myers, S. Welte, T. Moretti, T. McMahon, T. Grill, T. Kalafut, M. Greer-Ritzheimer, V. Beamer, D. A. Taylor, and J. S. Buckleton, "Internal validation of STRmix™ – A multi laboratory response to PCAST," *Forensic Sci. Int. Genet.*, vol. 34, no. January, pp. 11–24, 2018)].

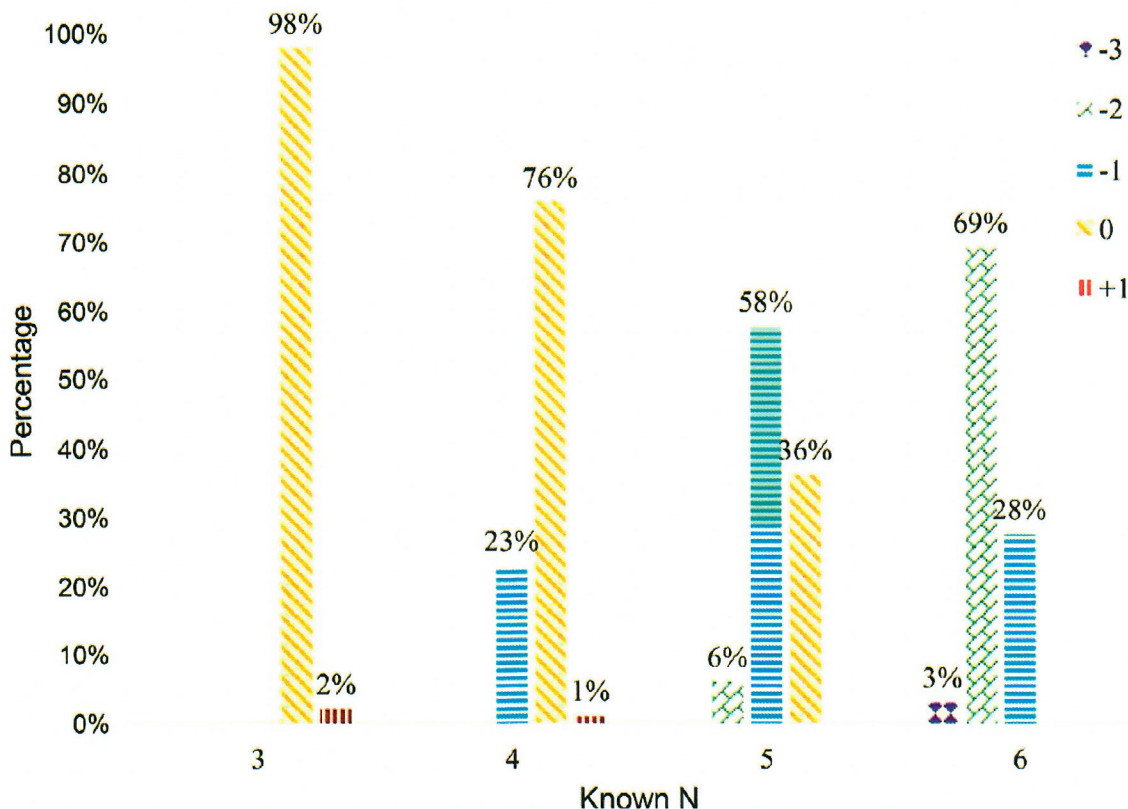


Figure 1 – Figure 13 from Bright, et al. – “Plot of percentage of mixtures showing various differences between apparent N and known N against known N. As an example, –1 indicates apparent N was one fewer than known N.”

14. Conceptual estimates from Coble, et al. and empirical data from Bright, et al.

demonstrate that the more known contributors to a sample, the more likely it is that an estimate of the number of contributors to that sample will be incorrect. Per Bright, et al., approximately 2/3 of evaluated known five-person mixtures and all evaluated known six-

person mixtures resulted in underestimates of the true number of contributors. Notably, the majority of known 4-, 5-, and 6-person mixtures were all estimated to contain DNA from four contributors.

15. The FBI's internal validation summary for STRmix™ v2.4 describes evaluating mixtures of up to four contributors. There is no indication that mixtures consisting of DNA from five or six individuals were evaluated. The FBI's internal validation study does state, "In sensitivity and specificity testing, most mixtures were assessed using different numbers of contributors," but gives no insight into the impact of incorrect assumptions of the number of contributors on the system's sensitivity or specificity for mixtures assumed to be 4-person mixtures. The validation summary also does not describe a rate at which incorrect assumptions were made by analysts blinded to the true number of contributors. If the laboratory has not evaluated 5-person mixtures, it can't be known at what rate analysts can accurately recognize samples that appear to be 4-person mixtures that are actually from 5-person mixtures, not 4-person mixtures.
16. A laboratory can evaluate at what rate an analyst (or the laboratory overall) correctly identifies known 5-person mixtures as 5-person mixtures or incorrectly characterizes them as 4-person mixtures. But, a laboratory cannot determine that a questioned/evidence sample that appears as if it could be from a 4-person mixture is not in fact from a 5-(or more) person mixture. Again, determining that a sample is from "at least four contributors" should not be construed as meaning that the sample is from "four contributors" or even "most likely four contributors." Given that Items 12 and 53 may be mixtures of DNA from five (or more) individuals it would be incorrect to treat them both as mixtures of four (and only four) individuals for the purposes of a STRmix™ analysis.

MIXTURE RATIOS

17. The FBI's internal validation summary for STRmix™ v2.4 describes evaluations of various mixture ratios for 2-, 3-, and 4- person mixtures. The ratios evaluated and their

corresponding contributor percentages are described in Table 1 below. The largest contribution by any single contributor was 58.8% and the lowest is 4.8%.

Ratio	Contributor 1	Contributor 2	Contributor 3	Contributor 4
10:5:5:1	47.6%	23.8%	23.8%	4.8%
10:5:1:1	58.8%	29.4%	5.9%	5.9%
5:5:1:1	41.7%	41.7%	8.3%	8.3%
1:1:1:1	25.0%	25.0%	25.0%	25.0%

Table 1 - Mixture ratios from Mixture Testing Summary supplement to "Validation of STRmix™ v2.4 for use with Globalfiler™ DNA Typing Results Generated on the 3500xL"

18. The STRmix™ deconvolution for item 12 reports mixture proportions of 55%, 26%, 15%, and 3%, for inferred contributors 1, 2, 3, and 4, respectively. 55% to 3% corresponds to a more extreme ratio (approximately 18:1) than the 10:1 ratio of the largest to smallest contributor amounts described in the FBI's internal validation study. Additionally, the 3% inferred contributor amount is less than the smallest proportion evaluated in known 4-person mixtures in the FBI's internal validation study.
19. The STRmix™ deconvolution for item 53 reports mixture proportions of 76%, 12%, 7%, and 5% for inferred contributors 1, 2, 3, and 4, respectively. Similar to item 12 (described in the previous paragraph), the ratio of the largest to smallest inferred contributor amounts (76% to 5%, approximately 15:1) is more extreme than the 10:1 ratio described in the FBI's internal validation study. The 76% inferred contributor amount is greater than the largest proportion evaluated in 4-person mixtures in the FBI's internal validation study.

SUMMARY AND CONCLUSIONS

20. It is common for mixtures known to contain DNA from five or more contributors to be mischaracterized as four-person mixtures using the methods that appear to have been relied upon by the FBI to determine the number of contributors to item 12 and item 53.

The FBI Casework Unit does not appear to have validated STRmix™ v2.4 for use with 5- or 6-person mixtures (including those that may have been mischaracterized as 4-person mixtures).

21. Mixture ratios investigated in the FBI's internal validation study of STRmix™ v2.4 are less extreme than the mixture ratios inferred by STRmix™ for genotyping results obtained from Items 12 and 53.

22. The FBI Casework Unit has not demonstrated that STRmix™ v2.4 can generate reliable results with evidence samples such as Items 12 and 53 in this case.

I declare, under penalty of perjury, that the foregoing is true and correct to the best of my knowledge.

Dated this 30th day of November 2018.

A handwritten signature in blue ink, appearing to read "Dan E. Krane", is written over a horizontal line.

Dan Krane, Ph.D.